

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/001,039BDATE: 05/11/2000
TIME: 18:16:21

INPUT SET: S35468.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANTS: Jolly, Douglas J.
6 Chang, Stephen M.W.
7 Respass, James G.
8 DePolo, Nicholas J.
9 Hsu, David Chi-Tang
10 Ibanez, Carlos E.
11 Greengard, Judith
12 Lee, Will
13
14 (ii) TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
15 RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
16 OF HEMOPHILIA AND OTHER DISORDERS
17
18 (iii) NUMBER OF SEQUENCES: 84
19
20 (iv) CORRESPONDENCE ADDRESS:
21 (A) ADDRESSEE: Seed Intellectual Property Law Group
22 (B) STREET: 701 Fifth Avenue, Suite 6300
23 (C) CITY: Seattle
24 (D) STATE: Washington
25 (E) COUNTRY: U.S.A.
26 (F) ZIP: 98104
27
28 (v) COMPUTER READABLE FORM:
29 (A) MEDIUM TYPE: Floppy disk
30 (B) COMPUTER: IBM PC compatible
31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
33
34 (vi) CURRENT APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 09/001,039
36 (B) FILING DATE: 13-JAN-1998
37 (C) CLASSIFICATION:
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: McMasters, David D.
41 (B) REGISTRATION NUMBER: 33,963
42 (C) REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (206) 622-4900
46 (B) TELEFAX: (206) 682-6031

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47
48
49
50 (2) INFORMATION FOR SEQ ID NO:1:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 24 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: DNA (genomic)
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58 GAGAGATGGG GGAGGCTAAC TGAG 24
59
60 (2) INFORMATION FOR SEQ ID NO:2:
61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 28 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear
66 (ii) MOLECULE TYPE: DNA (genomic)
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
68 GATCCTCAGT TAGCCTCCCC CATCTCTC 28
69
70 (2) INFORMATION FOR SEQ ID NO:3:
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 35 base pairs
73 (B) TYPE: nucleic acid
74 (C) STRANDEDNESS: single
75 (D) TOPOLOGY: linear
76 (ii) MOLECULE TYPE: DNA (genomic)
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
78 TATATCTCCA GATGAGGTAC ATGATTTTAG GCTTG 35
79
80 (2) INFORMATION FOR SEQ ID NO:4:
81 (i) SEQUENCE CHARACTERISTICS:
82 (A) LENGTH: 40 base pairs
83 (B) TYPE: nucleic acid
84 (C) STRANDEDNESS: single
85 (D) TOPOLOGY: linear
86 (ii) MOLECULE TYPE: DNA (genomic)
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
88 TATATATCGA TTCAAGGCAT TTTCTTTTCA TCAATAAAAC 40
89
90 (2) INFORMATION FOR SEQ ID NO:5:
91 (i) SEQUENCE CHARACTERISTICS:
92 (A) LENGTH: 37 base pairs
93 (B) TYPE: nucleic acid
94 (C) STRANDEDNESS: single
95 (D) TOPOLOGY: linear
96 (ii) MOLECULE TYPE: DNA (genomic)
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
98 TCGAGGATCC GCCCGGGCGG CCGCATCGAT GTCGACG 37
99

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100 (2) INFORMATION FOR SEQ ID NO:6:
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 35 base pairs
103 (B) TYPE: nucleic acid
104 (C) STRANDEDNESS: single
105 (D) TOPOLOGY: linear
106 (ii) MOLECULE TYPE: DNA (genomic)
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
108 CGCGTCGACA TCGATGCGGC CGCCCGGGCG GATCC 35
109
110
111 (2) INFORMATION FOR SEQ ID NO:7:
112 (i) SEQUENCE CHARACTERISTICS:
113 (A) LENGTH: 77 base pairs
114 (B) TYPE: nucleic acid
115 (C) STRANDEDNESS: single
116 (D) TOPOLOGY: linear
117 (ii) MOLECULE TYPE: DNA (genomic)
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
119 AGTGAATTCG AGCTCGGTAC CCGGGGATCC TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT 60
120 GCGGTACTCA TGGTCAT 77
121
122 (2) INFORMATION FOR SEQ ID NO:8:
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 8 amino acids
125 (B) TYPE: amino acid
126 (C) STRANDEDNESS: single
127 (D) TOPOLOGY: linear
128 (ii) MOLECULE TYPE: protein
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
130 Ala Arg Glu Met Gly Glu Ala Asn
131 1 5
132
133 (2) INFORMATION FOR SEQ ID NO:9:
134 (i) SEQUENCE CHARACTERISTICS:
135 (A) LENGTH: 27 base pairs
136 (B) TYPE: nucleic acid
137 (C) STRANDEDNESS: single
138 (D) TOPOLOGY: linear
139 (ii) MOLECULE TYPE: DNA (genomic)
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
141 CCCGAGAGAT GGGGGAGGCT AACTGAG 27
142
143 (2) INFORMATION FOR SEQ ID NO:10:
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 31 base pairs
146 (B) TYPE: nucleic acid
147 (C) STRANDEDNESS: single
148 (D) TOPOLOGY: linear
149 (ii) MOLECULE TYPE: DNA (genomic)
150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
151 GGGCTCTCTA CCCCTCCGA TTGACACCTA G 31
152

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153 (2) INFORMATION FOR SEQ ID NO:11:
154 (i) SEQUENCE CHARACTERISTICS:
155 (A) LENGTH: 5 amino acids
156 (B) TYPE: amino acid
157 (C) STRANDEDNESS: single
158 (D) TOPOLOGY: linear
159 (ii) MOLECULE TYPE: protein
160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
161 Thr Ile Met Thr Met
162 1 5
163
164
165 (2) INFORMATION FOR SEQ ID NO:12:
166 (i) SEQUENCE CHARACTERISTICS:
167 (A) LENGTH: 24 base pairs
168 (B) TYPE: nucleic acid
169 (C) STRANDEDNESS: single
170 (D) TOPOLOGY: linear
171 (ii) MOLECULE TYPE: DNA (genomic)
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
173 CCCTGTGCCT TATTTGAACT AACC 24
174
175 (2) INFORMATION FOR SEQ ID NO:13:
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 24 base pairs
178 (B) TYPE: nucleic acid
179 (C) STRANDEDNESS: single
180 (D) TOPOLOGY: linear
181 (ii) MOLECULE TYPE: DNA (genomic)
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
183 CCCACCACAA CCACATATCC CTCC 24
184
185 (2) INFORMATION FOR SEQ ID NO:14:
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 19 base pairs
188 (B) TYPE: nucleic acid
189 (C) STRANDEDNESS: single
190 (D) TOPOLOGY: linear
191 (ii) MOLECULE TYPE: DNA (genomic)
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
193 CCAGTCCTCC GATTGACTG 19
194
195 (2) INFORMATION FOR SEQ ID NO:15:
196 (i) SEQUENCE CHARACTERISTICS:
197 (A) LENGTH: 8332 base pairs
198 (B) TYPE: nucleic acid
199 (C) STRANDEDNESS: single
200 (D) TOPOLOGY: linear
201 (ii) MOLECULE TYPE: DNA (genomic)
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
203
204 GCGCCAGTCC TCCGATTGAC TGAGTCGCCC GGTACCCGT GTATCCAATA AACCTCTTG 60
205

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206	CAGTTGCATC	CGACTTGTGG	TCTCGCTGTT	CCTTGGGAGG	GTCTCCTCTG	AGTGATTGAC	120
207							
208	TACCCGTCAG	CGGGGGTCTT	TCATTGTTGGG	GCTCGTCCGG	GATCGGGAGA	CCCCTGCCCA	180
209							
210	GGGACCACCG	ACCCACCACC	GGGAGGTAAG	CTGGCCAGCA	ACTTATCTGT	GTCTGTCCGA	240
211							
212	TTGTCTAGTG	TCTATGACTG	ATTTTATGCG	CCTGCGTCGG	TACTAGTTAG	CTAACTAGCT	300
213							
214	CTGTATCTGG	CGGACCCGTG	GTGGAAGTGA	CGAGTTCGGA	ACACCCGGCC	GCAACCCCTGG	360
215							
216	GAGACGTCCC	AGGGACTTCG	GGGGCCGTTT	TTGTGGCCCC	ACCTGAGTCC	AAAAATCCCC	420
217							
218	ATCGTTTTGG	ACTCTTTGGT	GCACCCCCCT	TAGAGGAGGG	ATATGTGGTT	CTGGTAGGAG	480
219							
220	ACGAGAACCT	AAACAGTTC	CCGCCTCCGT	CTGAATTTTT	GCTTTCGGTT	TGGGACCGAA	540
221							
222	GCCGCGCCGC	GCGTCTTGTC	TGCTGCAGCA	TCGTTCTGTG	TTGTCTCTGT	CTGACTGTGT	600
223							
224	TTCTGTATTT	GTCTGAGAAT	ATGGGCCAGA	CTGTTACCAC	TCCCTTAAGT	TTGACCTTAG	660
225							
226	GTCAGTGAA	AGATGTCGAG	CGGATCGCTC	ACAACCAGTC	GGTAGATGTC	AAGAAGAGAC	720
227							
228	GTTGGGTTAC	CTTCTGCTCT	GCAGAAATGGC	CAACCTTTAA	CGTCGGATGG	CCGCGAGACG	780
229							
230	GCACCTTTAA	CCGAGACCTC	ATCACCCAGG	TTAAGATCAA	GGTCTTTTCA	CCTGGCCCCG	840
231							
232	ATGGACACCC	AGACCAGGTC	CCCTACATCG	TGACCTGGGA	AGCCTTGGCT	TTTGACCCCC	900
233							
234	CTCCCTGGGT	CAAGCCCTTT	GTACACCCTA	AGCCTCCGCC	TCCTCTTCCT	CCATCCGCCC	960
235							
236	CGTCTCTCCC	CCTTGAACCT	CCTCGTTCGA	CCCCGCCTCG	ATCCTCCCTT	TATCCAGCCC	1020
237							
238	TCACTCCTTC	TCTAGGCGCC	AAACCTAAAC	CTCAAGTTCT	TTCTGACAGT	GGGGGGCCGC	1080
239							
240	TCATCGACCT	ACTTACAGAA	GACCCCCCGC	CTTATAGGGA	CCCAAGACCA	CCCCCTTCCG	1140
241							
242	ACAGGGACGG	AAATGGTGGA	GAAGCGACCC	CTGCGGGAGA	GGCACC GGAC	CCCTCCCCAA	1200
243							
244	TGGCATCTCG	CCTACGTGGG	AGACGGGAGC	CCCCTGTGGC	CGACTCCACT	ACCTCGCAGG	1260
245							
246	CATTCCCCCT	CCGCGCAGGA	GGAAACGGAC	AGCTTCAATA	CTGGCCGTTC	TCCTCTTCTG	1320
247							
248	ACCTTTACAA	CTGGAAAAAT	AATAACCCCT	CTTTTTCTGA	AGATCCAGGT	AAACTGACAG	1380
249							
250	CTCTGATCGA	GTCTGTTCTC	ATCACCCATC	AGCCACCTG	GGACGACTGT	CAGCAGCTGT	1440
251							
252	TGGGGACTCT	GCTGACCGGA	GAAGAAAAAC	AACGGGTGCT	CTTAGAGGCT	AGAAAGGCGG	1500
253							
254	TGCGGGGCGA	TGATGGGCGC	CCCACTCAAC	TGCCCAATGA	AGTCGATGCC	GCTTTTCCCC	1560
255							
256	TCGAGCGCCC	AGACTGGGAT	TACACCACCC	AGGCAGGTAG	GAACCACCTA	GTCCACTATC	1620
257							
258	GCCAGTTGCT	CCTAGCGGGT	CTCCAAAACG	CGGGCAGAAG	CCCCACCAAT	TTGGCCAAGG	1680

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